

SEQUENCE LISTING

<110> Ernst-Moritz-Arndt University Greifswald

<120> Use of the Multifunctional Transcription Factor Yin Yang 1 and Variants Thereof for Treating Illnesses, Especially Type 1 Diabetes

<130> P 62096

<160> 8

<170> PatentIn version 3.1

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<212> DNA

<213> Rattus norv.

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<221> CDS

<222> (73)..(1125)

<223> YY1 (BB/OK)

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<222> (1759)..(1917)

<223> Zinc finger

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      1          5          10

tcg gag atg cca gcc gag atc gtg gaa ctg cat gag att gag gtg gag 159
Ser Glu Met Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu
      15          20          25

acc atc ccg gtg gag act atc gag acc acg gtg gtg ggc gag gag gag 207
Thr Ile Pro Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu
      30          35          40          45

gac gac gac gaa gac gac gag gat ggt ggc ggc gga gac cac ggt ggc 255
Asp Asp Asp Glu Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly
      50          55          60

ggg ggc ggc cac ggc cac gct ggc cac cac cat cac cac cac cac cac 303
Gly Gly Gly His Gly His Ala Gly His His His His His His His His
      65          70          75

cac cac ccg ccc atg atc gcg ctg cag ccg ctg gtc acc gac gac ccg 351
His His Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro
      80          85          90

acc caa gtg cac cac cac caa gag gtg att ctg gtg cag acg cgc gag 399
Thr Gln Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu
      95          100          105

gag gta gtg ggt ggc gac gac tcg gac ggc ctg cgc gcc gag gac ggc 447
Glu Val Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly
      110          115          120          125

ttc gag gac cag atc ctc att ccg gta ccc gcg ccg gcc ggc gga gac 495
Phe Glu Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp
      130          135          140

gac gac tac atc gag cag acg ctg gtc acc gtg gcg gcg gcc ggc aag 543
Asp Asp Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys
      145          150          155

agc ggt ggc ggc tct tcg tcg ggc ggc ggc cgc gtt aag aag ggc ggc 591
Ser Gly Gly Gly Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly
      160          165          170

ggc aag aag agc ggc aag aag agt tac ctg ggc agc ggc gcc ggc gcg 639
Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Gly Ser Gly Ala Gly Ala
      175          180          185

gcg ggc ggt ggc ggc gcc gac ccg ggt aat aag aag tgg gaa cag aag 687
Ala Gly Gly Gly Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys
      190          195          200          205

cag gtg cag atc aag acc ctg gag ggc gag ttc tcg gtc acc atg tgg 735
Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp
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tct tca gat gaa aaa aaa gat att gac cat gaa aca gtg gtt gaa gag Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu 225 230 235	783
cag atc att ggg gag aac tca cct cct gat tat tct gaa tat atg aca Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr 240 245 250	831
ggc aag aaa ctc cct cct gga ggg ata cct ggc att gac ctc tca gac Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp 255 260 265	879
ccc aag caa ctg gca gaa ttt gcc aga atg aag cca aga aaa att aaa Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys 270 275 280 285	927
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tgcttgggtt cctgggttact gctcgggact gcagggtgtta cagatggggg tggagggatt	1295
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tctcatattgc caagaggggt gatatctgg ttttccttga cag tgc aca ttc gaa Cys Thr Phe Glu 355	1770

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 Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg Thr His Val
 360 365 370

cga atc cat acc gga gac agg ccc tat gtg tgc ccc ttc gac ggt tgt 1866
 Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe Asp Gly Cys
 375 380 385

aat aag aag ttt gct cag tca act aac ctg aaa tct cac atc tta aca 1914
 Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His Ile Leu Thr
 390 395 400

cac gct aaa gcc aaa aac aac cag tgaaaagaag agagaagacc ttctcgaccc 1968
 His Ala Lys Ala Lys Asn Asn Gln
 405 410

cggaagcct cttcaggagt gtgattggga ataaatatgc ctctcctttg tatattat 2028

ctaggaagaa ttttaaaaat gaatcctaca cacttaaggg acatgttttg ataaagtagt 2088

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 <223> Zinc finger

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Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro
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Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Asp Asp Asp
 35 40 45

Glu Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly
 50 55 60

His	Gly	His	Ala	Gly	His	His	His	His	His	His	His	His	His	His	Pro	65	70	75	80
Pro	Met	Ile	Ala	Leu	Gln	Pro	Leu	Val	Thr	Asp	Asp	Pro	Thr	Gln	Val	85	90	95	
His	His	His	Gln	Glu	Val	Ile	Leu	Val	Gln	Thr	Arg	Glu	Glu	Val	Val	100	105	110	
Gly	Gly	Asp	Asp	Ser	Asp	Gly	Leu	Arg	Ala	Glu	Asp	Gly	Phe	Glu	Asp	115	120	125	
Gln	Ile	Leu	Ile	Pro	Val	Pro	Ala	Pro	Ala	Gly	Gly	Asp	Asp	Asp	Tyr	130	135	140	
Ile	Glu	Gln	Thr	Leu	Val	Thr	Val	Ala	Ala	Ala	Gly	Lys	Ser	Gly	Gly	145	150	155	160
Gly	Ser	Ser	Ser	Gly	Gly	Gly	Arg	Val	Lys	Lys	Gly	Gly	Gly	Lys	Lys	165	170	175	
Ser	Gly	Lys	Lys	Ser	Tyr	Leu	Gly	Ser	Gly	Ala	Gly	Ala	Ala	Gly	Gly	180	185	190	
Gly	Gly	Ala	Asp	Pro	Gly	Asn	Lys	Lys	Trp	Glu	Gln	Lys	Gln	Val	Gln	195	200	205	
Ile	Lys	Thr	Leu	Glu	Gly	Glu	Phe	Ser	Val	Thr	Met	Trp	Ser	Ser	Asp	210	215	220	
Glu	Lys	Lys	Asp	Ile	Asp	His	Glu	Thr	Val	Val	Glu	Glu	Gln	Ile	Ile	225	230	235	240
Gly	Glu	Asn	Ser	Pro	Pro	Asp	Tyr	Ser	Glu	Tyr	Met	Thr	Gly	Lys	Lys	245	250	255	
Leu	Pro	Pro	Gly	Gly	Ile	Pro	Gly	Ile	Asp	Leu	Ser	Asp	Pro	Lys	Gln	260	265	270	
Leu	Ala	Glu	Phe	Ala	Arg	Met	Lys	Pro	Arg	Lys	Ile	Lys	Glu	Asp	Asp	275	280	285	
Ala	Pro	Arg	Thr	Ile	Ala	Cys	Pro	His	Lys	Gly	Cys	Thr	Lys	Met	Phe	290	295	300	

Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His Gly Pro Arg
 305 310 315 320

Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu Ser Ser Lys
 325 330 335

Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro Phe Gln Cys
 340 345 350

Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg
 355 360 365

Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe
 370 375 380

Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His
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Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
 405 410

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 <222> (73)..(1125)
 <223> YY1 (SHR)

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 Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly
 1 5 10

tcg gag atg cca gcc gag atc gtg gaa ctg cat gag att gag gtg gag 159
 Ser Glu Met Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu
 15 20 25

acc atc ccg gtg gag act atc gag acc acg gtg gtg ggc gag gag gag 207
 Thr Ile Pro Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu
 30 35 40 45

gac gac gac gaa gac gac gag gat ggt ggc ggc gga gac cac ggt ggc 255
 Asp Asp Asp Glu Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly
 50 55 60

ggg ggc ggc cac ggg cac gct ggc cac cac cat cac cac cac cac cac 303
 Gly Gly Gly His Gly His Ala Gly His His His His His His His
 65 70 75

cac cac ccg ccc atg atc gcg ctg cag ccg ctg gtc acc gac gac ccg 351
 His His Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro
 80 85 90

acc caa gtg cac cac cac caa gag gtg att ctg gtg cag acg cgc gag 399
 Thr Gln Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu
 95 100 105

gag gta gtg ggt ggc gac gac tcg gac ggg ctg cgc gcc gag gac ggg 447
 Glu Val Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly
 110 115 120 125

ttc gag gac cag atc ctc att ccg gta ccc gcg ccg gcc ggc gga gac 495
 Phe Glu Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp
 130 135 140

gac gac tac atc gag cag acg ctg gtc acc gtg gcg gcg gcc ggc aag 543
 Asp Asp Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys
 145 150 155

agc ggt ggc ggg tct tcg tcg ggc ggc ggc cgc gtt aag aag ggc ggc 591
 Ser Gly Gly Gly Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly
 160 165 170

ggc aag aag agt ggc aag aag agt tac ctg ggc agc ggg gcc ggc gcg 639
 Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Gly Ser Gly Ala Gly Ala
 175 180 185

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aag agg ttc agg gat aac tct gct atg aaa aag cat ctg cac acc cac Lys Arg Phe Arg Asp Asn Ser Ala Met Lys Lys His Leu His Thr His 305 310 315	1023
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ccaggtgaca cttgggtgctg cttatagaag acacgtgagt tgacagttgg catcactaaa	1475
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ttgcactcag cacagccctt ctgtttctca agaactagcc atgggttggt agtatcagag	1595
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tctcatttgc caagagggtt gatatctggt ttttccttga cag tgc aca ttc gaa 1770
                                Cys Thr Phe Glu
                                355

ggc tgc ggg aag cgc ttt tca ctg gac ttc aat ttg cgc acg cat gtg 1818
Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg Thr His Val
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cga atc cat acc gga gac agg ccc tat gtg tgc ccc ttc gac ggt tgt 1866
Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe Asp Gly Cys
                                375                380                385

aat aag aag ttt gct cag tca act aac ctg aaa tct cac atc tta aca 1914
Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His Ile Leu Thr
                                390                395                400

cac gct aaa gcc aaa aac aac cag tgaaaagaag agagaagacc ttctcgaccc 1968
His Ala Lys Ala Lys Asn Asn Gln
                                405                410

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ctaggaagaa ttttaaaaat gaatcctaca cacttaaggg acatgttttg ataaagtagt 2088
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Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Asp Asp Asp
35          40          45

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Glu Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly
 50 55 60

His Gly His Ala Gly His His His His His His His His His His His Pro
 65 70 75 80

Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln Val
 85 90 95

His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val Val
 100 105 110

Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu Asp
 115 120 125

Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp Tyr
 130 135 140

Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly Gly
 145 150 155 160

Gly Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly Gly Lys Lys
 165 170 175

Ser Gly Lys Lys Ser Tyr Leu Gly Ser Gly Ala Gly Ala Ala Gly Gly
 180 185 190

Gly Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys Gln Val Gln
 195 200 205

Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp Ser Ser Asp
 210 215 220

Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu Gln Ile Ile
 225 230 235 240

Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr Gly Lys Lys
 245 250 255

Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp Pro Lys Gln
 260 265 270

Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys Glu Asp Asp
 275 280 285

Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr Lys Arg Phe
290 295 300

Arg Asp Asn Ser Ala Met Lys Lys His Leu His Thr His Gly Pro Arg
305 310 315 320

Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu Ser Ser Lys
325 330 335

Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro Phe Gln Cys
340 345 350

Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg
355 360 365

Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe
370 375 380

Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His
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Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
405 410

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Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met Pro Ala Glu Ile
5 10 15 20

gtg gag ctg cat gag atc gag gtg gag acc atc ccg gtg gag acc atc 150
Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro Val Glu Thr Ile
25 30 35

gag acc acg gtg gtg ggc gag gag gag gag gag gac gac gac gac gag	198
Glu Thr Thr Val Val Gly Glu Glu Glu Glu Glu Asp Asp Asp Asp Glu	
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gac ggc ggc ggc ggc gac cac ggc ggc ggc ggg ggc ggc cac ggg cac	246
Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly Gly His Gly His	
55 60 65	
gcc ggc cac cac cat cac cac cac cac cac cac cac cac ccg ccc	294
Ala Gly His His His His His His His His His His His His Pro Pro	
70 75 80	
atg atc gcg ctg gag ccg ctg gtg acg gac gac ccg acc caa gtg cac	342
Met Ile Ala Leu Glu Pro Leu Val Thr Asp Asp Pro Thr Gln Val His	
85 90 95 100	
cac ctc cag gag gtg atc ctg gtg cag acg cgc gag gag gtc gtc ggg	390
His Leu Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val Val Gly	
105 110 115	
ggg gac gac tcg gac ggc ctg cgc gcc gag gac ggc ttc gag gac gag	438
Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu Asp Glu	
120 125 130	
atc ctc atc ccg gtg ccc gcg ccg gcc ggc ggc gac gac gac tac ata	486
Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp Tyr Ile	
135 140 145	
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Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly Gly Gly	
150 155 160	
gcc tcg tcg ggc ggc ggt cgc gtg aag aag ggc ggc ggc aag aag agc	582
Ala Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly Gly Lys Lys Ser	
165 170 175 180	
ggc aag aag agt tac ctg ggc ggc ggg gcc ggc gcg gcg ggc ggc ggc	630
Gly Lys Lys Ser Tyr Leu Gly Gly Gly Ala Gly Ala Ala Gly Gly Gly	
185 190 195	
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Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys Gln Val Gln Ile	
200 205 210	
aag acc ctg gag ggc gag tcc tcg gtc acc atg tgg tcc tcg gat gaa	726
Lys Thr Leu Glu Gly Glu Ser Ser Val Thr Met Trp Ser Ser Asp Glu	
215 220 225	
aaa aaa gat att gac cat gaa aca gtg gtt gaa gag cag atc att gga	774
Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu Gln Ile Ile Gly	
230 235 240	
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Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr Gly Lys Lys Leu	
245 250 255 260	
cct cct gga ggg ata cct ggc att gac ctc tca gac cct aag caa ctg	870
Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp Pro Lys Gln Leu	
265 270 275	

gca gaa ttt gcc aga atg aag cca aga aaa att aaa gaa gat gat gct 918
 Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys Glu Asp Asp Ala
 280 285 290

cca aga aca ata gct tgc cct cat aaa ggc tgc aca aag atg ttc agg 966
 Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr Lys Met Phe Arg
 295 300 305

gat aac tct gct atg aga aag cat ctg cac acc cac ggt ccc aga gtc 1014
 Asp Asn Ser Ala Met Arg Lys His Leu His Thr His Gly Pro Arg Val
 310 315 320

cac gtc tgt gca gag tgt ggc aaa gcg ttc gtt gag agc tca aag cta 1062
 His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu Ser Ser Lys Leu
 325 330 335 340

aaa cga cac cag ctg gtt cat act gga gaa aag ccc ttt cag tgc aca 1110
 Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro Phe Gln Cys Thr
 345 350 355

ttc gaa ggc tgc ggg aag cgc ttt tca ctg gac ttc aat ttg cgc aca 1158
 Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg Thr
 360 365 370

cat gtg gga atc cat acc gga gac agg ccc tat gtg tgc ccc ttc gac 1206
 His Val Gly Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe Asp
 375 380 385

ggt tgt aat aag aag ttt gct cag tca act aac ctg aaa tct cac atc 1254
 Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His Ile
 390 395 400

tta aca cac gct aaa gcc aaa aac aac cag tgaaaagaag agagaagacc 1304
 Leu Thr His Ala Lys Ala Lys Asn Asn Gln
 405 410

ttctcgaccc gggaagcctc ttcaggagtg agattgggaa taaatatgcc tctcctttgt 1364

atattatttc taggaagaat tttaaaaatg aatcctacac acttaaggga catgttttga 1424

taaagtagta aaaattttaa aaatacttta ataagatgac attgctaaga tgctatatct 1484

tgctctgtaa tctcgtttca aaaacaaggt gtttttgtaa agtgtggtcc caacaggagg 1544

acaattcatg aacttcgcat caaaagacaa ttcttttatac aacagtgcta aaaatg 1600

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 <211> 414
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met
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Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro
 20 25 30

Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Glu Asp
 35 40 45

Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly
 50 55 60

Gly His Gly His Ala Gly His His His His His His His His His His
 65 70 75 80

His His Pro Pro Met Ile Ala Leu Glu Pro Leu Val Thr Asp Asp Pro
 85 90 95

Thr Gln Val His His Leu Gln Glu Val Ile Leu Val Gln Thr Arg Glu
 100 105 110

Glu Val Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly
 115 120 125

Phe Glu Asp Glu Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp
 130 135 140

Asp Asp Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys
 145 150 155 160

Ser Gly Gly Gly Ala Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly
 165 170 175

Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Gly Gly Gly Ala Gly Ala
 180 185 190

Ala Gly Gly Gly Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys
 195 200 205

Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Ser Ser Val Thr Met Trp
 210 215 220

Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu
 225 230 235 240

Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr
 245 250 255

Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp
 260 265 270

Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys
 275 280 285

Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr
 290 295 300

Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His
 305 310 315 320

Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu
 325 330 335

Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro
 340 345 350

Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe
 355 360 365

Asn Leu Arg Thr His Val Gly Ile His Thr Gly Asp Arg Pro Tyr Val
 370 375 380

Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu
 385 390 395 400

Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
 405 410

<210> 7
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 <212> DNA
 <213> Rattus norv.

<220>
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 <222> (883)..(894)
 <223> Shortened zinc finger (BB.6S)

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 <223> Shortened zinc finger (BB.6S)

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gtgggcgagg aggaggacga cgacgaagac gacgaggatg gtggcgggcg agaccacggt 180
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gaggtgattc tgggtgcagac gcgcgaggag gtagtgggtg gcgacgactc ggacgggctg 360
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ggggagaact cacctcctga ttattctgaa tatatgacag gcaagaaact ccctcctgga 780
gggatacctg gcattgacct ctgagacccc aagcaactgg cagaatttgc cagaatgaag 840
ccaagaaaaa ttaaagaaga tgatgctcca agaacaatag ct tgc cct cat aaa 894

Cys Pro His Lys
1

cag tgc aca ttc gaa ggc tgc ggg aag cgc ttt tca ctg gac ttc aat 942
Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn
5 10 15

ttg cgc acg cat gtg cga atc cat acc gga gac agg ccc tat gtg tgc 990
Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys
20 25 30 35

ccc ttc gac ggt tgt aat aag aag ttt gct cag tca act aac ctg aaa 1038
Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys
40 45 50

tct cac atc tta aca cac gctaaagcca aaaacaacca gtga 1080
Ser His Ile Leu Thr His
55

<210> 8
<211> 57
<212> PRT
<213> Rattus norv.

<400> 8

Cys Pro His Lys Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu
1 5 10 15

Asp Phe Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro
20 25 30

Tyr Val Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr
35 40 45

Asn Leu Lys Ser His Ile Leu Thr His
50 55